



SEQUENCE LISTING

<110> PARANHOS-BACCALA, Glaucia

KOMURIAN-PRADEL, Florence

BEDIN, Frederic

SODOYER, Mireille

OTT, Catherine

MALLET, Francois

PERRON, Herve

MANDRAND, Bernard

<120> RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES

<130> 103514

<140> US/09/319,156

<141> 1999-11-02

<150> PCT/FR98/01460

<151> 1998-07-07

<150> FR/97/08816

<151> 1997-07-07

<160> 45

<170> PatentIn version 3.1

RECEIVED

NOV 20 2001

TECH CENTER 1600/2900

<210> 1  
<211> 34  
<212> DNA  
<213> MSRV

<400> 1  
gactcgctgc agatcgattt tttttttttt tttt 34

<210> 2  
<211> 30  
<212> DNA  
<213> MSRV

<400> 2  
gccatcaagc cacccaagaa ctcttaactt 30

<210> 3  
<211> 30  
<212> DNA  
<213> MSRV

<400> 3  
ccaatagcca gaccattata tacactaatt 30

<210> 4  
<211> 310  
<212> DNA  
<213> MSRV

<400> 4  
gcttatagaa ggacccctag tatggggtaa tcccctctgg gaaaccaagc cccagttactc 60  
agcaggaaaa atagaatagg aaacacctaca aggacatact ttcctccctt ccagatggct 120  
agccactgag gaaggaaaaa tactttcacc tgcagctaac caacagaaat tacttaaaac 180

ccttcaccaa accttccact taggcattga tagcacccat cagatggcca aattattatt 240  
tactggacca ggcctttca aaactatcaa gaagatagtc aggggctgtg aagtgtgcc 300  
aagaaaataat 310

<210> 5

<211> 103

<212> PRT

<213> MSRV

<220>

<221> misc\_feature

<222> (26)..(26)

<223> Xaa = any amino acid

<400> 5

Leu Ile Glu Gly Pro Leu Val Trp Gly Asn Pro Leu Trp Glu Thr Lys  
1 5 10 15

Pro Gln Tyr Ser Ala Gly Lys Ile Glu Xaa Glu Thr Ser Gln Gly His  
20 25 30

Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu  
35 40 45

Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr  
50 55 60

Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe  
65 70 75 80

Thr Gly Pro Gly Leu Phe Lys Thr Ile Lys Lys Ile Val Arg Gly Cys  
85 90 95

Glu Val Cys Gln Arg Asn Asn  
100

<210> 6  
<211> 635  
<212> DNA  
<213> MSRV

<400> 6  
ccctgtatct ttaacccct tgttaagttt gtctttcca gaatcaaaac tgtaaaacta 60  
caaattgttc ttcaaatgga gcaccagatg gagtccatga ctaagatcca ccgtggaccc 120  
ctggaccggc ctgctagccc atgctccgat gttaatgaca ttgaaggcac ccctcccgag 180  
gaaatctcaa ctgcacaacc cctactatgc cccattcag cggaaagcag ttagagcggt 240  
catcagccaa cctcccaac agcacttggg tttcctgtt gagagggggg actgagagac 300  
aggactagct ggatttccta ggccaaacgaa gaatccctaa gcctagctgg gaaggtgact 360  
gcatccacct ctaaacatgg ggcttgcaac ttagctcaca cccgaccaat cagagagctc 420  
actaaaatgc taattaggca aaaataggag gtaaagaaat agccaatcat ctattgcctg 480  
agagcacagc gggagggaca aggatcgggataaaaccca ggcattcgag ccggcaacgg 540  
caacccccc tgggtccctt ccctttgtat gggcgctctg tttcactct atttcactct 600  
attaaatctt gcaactgaaa aaaaaaaaaa aaaaa 635

<210> 7  
<211> 77  
<212> PRT  
<213> MSRV

<400> 7  
Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile Lys  
1 5 10 15  
Thr Val Lys Leu Gln Ile Val Leu Gln Met Glu His Gln Met Glu Ser  
20 25 30  
Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys  
35 40 45

Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr  
50 55 60

Ala Gln Pro Leu Leu Cys Pro Asn Ser Ala Gly Ser Ser  
65 70 75

<210> 8

<211> 32

<212> DNA

<213> MSRV

<400> 8

tggggttcca tttgtaagac catctgttagc tt

32

<210> 9

<211> 1481

<212> DNA

<213> MSRV

<400> 9

atggccctcc cttatcatac ttttctcttt actgttctct taccccttt cgctctcact 60

gcaccccttc catgctgctg tacaaccagt agctccctt accaagagtt tctatgaaga 120

acgcggcttc ctggaaatat tcatatccatata gtttatctaa gggaaactcc 180

accttcactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatt 240

catgcaaata ctcattattt gacagggaaa atgattaatc ctagttgtcc tggaggactt 300

ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg gggtgaaatt 360

caaggtcagg caagagaaaa acaagtaaag gaagcaatct cccaaactgac ccggggacat 420

agcaccccta gcccctacaa aggactagtt ctctaaaaac tacatgaaac cctccgtacc 480

catactcgcc tggtgagcct atttaataacc accctcactc ggctccatga ggtctcagcc 540

caaaacccta ctaactgttg gatgtgcctc cccctgcact tcaggccata catttcaatc 600

cctgttcctg aacaatggaa caacttcagc acagaaataa acaccacttc cgtttttagta 660

ggacctcttg tttccaatct ggaaataacc catacctcaa acctcacctg tgtaaaattt 720

agcaatacta tagacacaac cagctcccaa tgcacatcagg ggtaacacc tcccacacga 780

atagtctgcc taccctcagg aatattttt gtctgtggta cctcagccta tcattgtttg 840  
aatggctctt cagaatctat gtgcttcctc tcattcttag tgccccctat gaccatctac 900  
actgaacaag atttatacaa tcatgtcgta cctaagcccc acaacaaaag agtaccatt 960  
cttccttttgc ttatcagagc aggagtgcta ggcagactag gtactggcat tggcagttac 1020  
acaacctcta ctcagttcta ctacaaacta tctcaagaaa taaatggta catgaaacag 1080  
gtcactgact ccctggtcac cttgcaagat caacttaact ccctagcagc agtagtcctt 1140  
caaaatcgaa gagctttaga cttgctaacc gccaaaagag gggaaacctg tttatttta 1200  
ggagaagaac gctgttatta tgttaatcaa tccagaatttgc tcactgagaa agttaaagaa 1260  
attcgagatc gaatacaatg tagagcagag gagcttcaaa acaccgaacg ctggggcctc 1320  
ctcagccaat ggatgccctg ggttctcccc ttcttaggac ctctagcagc tctaataatttgc 1380  
ttactcctct ttggaccctg tatcttaac ctccttggta agttgtctc ttccagaatttgc 1440  
gaagctgtaa agctacagat ggtcttacaa atggaaccccc a 1481

<210> 10

<211> 493

<212> PRT

<213> MSRV

<220>

<221> misc\_feature

<222> (39)..(39)

<223> Xaa = any amino acid

<400> 10

Met Ala Leu Pro Tyr His Thr Phe Leu Phe Thr Val Leu Leu Pro Pro  
1 5 10 15

Phe Ala Leu Thr Ala Pro Pro Pro Cys Cys Cys Thr Thr Ser Ser Ser  
20 25 30

Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp  
35 40 45

Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala  
50 55 60

His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met  
65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys  
85 90 95

Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr  
100 105 110

Ser Met Ser Asp Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln  
115 120 125

Val Lys Glu Ala Ile Ser Gln Leu Thr Arg Gly His Ser Thr Pro Ser  
130 135 140

Pro Tyr Lys Gly Leu Val Leu Ser Lys Leu His Glu Thr Leu Arg Thr  
145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Arg Leu His  
165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Met Cys Leu Pro Leu  
180 185 190

His Phe Arg Pro Tyr Ile Ser Ile Pro Val Pro Glu Gln Trp Asn Asn  
195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val  
210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe  
225 230 235 240

Ser Asn Thr Ile Asp Thr Thr Ser Ser Gln Cys Ile Arg Trp Val Thr  
245 250 255

Pro Pro Thr Arg Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys  
260 265 270

Gly Thr Ser Ala Tyr His Cys Leu Asn Gly Ser Ser Glu Ser Met Cys  
275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp  
290 295 300

Leu Tyr Asn His Val Val Pro Lys Pro His Asn Lys Arg Val Pro Ile  
305 310 315 320

Leu Pro Phe Val Ile Arg Ala Gly Val Leu Gly Arg Leu Gly Thr Gly  
325 330 335

Ile Gly Ser Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln  
340 345 350

Glu Ile Asn Gly Asp Met Glu Gln Val Thr Asp Ser Leu Val Thr Leu  
355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg  
370 375 380

Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr Cys Leu Phe Leu  
385 390 395 400

Gly Glu Glu Arg Cys Tyr Tyr Val Asn Gln Ser Arg Ile Val Thr Glu  
405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Cys Arg Ala Glu Glu Leu  
420 425 430

Gln Asn Thr Glu Arg Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Val  
435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Phe  
450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile  
465 470 475 480

Glu Ala Val Lys Leu Gln Met Val Leu Gln Met Glu Pro  
485 490

<211> 32

<212> DNA

<213> MSRV

<400> 11

tcaaaaatcga agagctttag acttgctaac cg

32

<210> 12

<211> 1329

<212> DNA

<213> MSRV

<220>

<221> misc\_feature

<222> (594)..(594)

<223> n = a, g, c or t/u

<220>

<221> misc\_feature

<222> (602)..(602)

<223> n = a, g, c or t/u

<220>

<221> misc\_feature

<222> (1232)..(1232)

<223> n = a, g, c or t/u

<400> 12

tcaaaaatcga agagctttag acttgctaac cgccaaaaga gggggAACCT gtttattttt

60

aggggaagaa tgctgttagt atgttaatca atctggaatc attactgaga aagttaaaga

120

aatttgagat cgaatataat gtagagcaga ggaccttcaa aacactgcac cctggggcct

180

cctcagccaa tggatgccct ggactctccc cttcttagga cctcttagcag ctataatatt	240
tttactcctc tttggaccct gtatcttcaa cttccttgtt aagtttgcct cttccagaat	300
tgaagctgta aagctacaaa tagttctca aatggAACCC cagatgcagt ccatgactaa	360
aatctaccgt ggacccctgg accggcctgc tagactatgc tctgatgtta atgacattga	420
agtcacccct cccgaggaaa tctcaactgc acaaccccta ctacactcca attcagtagg	480
aagcagttag agcagttgtc agccaacctc cccaacagta cttgggttt cctgttgaga	540
gggtggactg agagacagga ctagctggat ttccttaggct gactaagaat cccnaagcct	600
anctgggaag gtgaccgcat ccatcttaa acatggggct tgcaacttag ctcacacccg	660
accaatcaga gagctcacta aaatgcta caggcaaaaa caggaggtaa agcaatagcc	720
aatcatctat tgcctgagag cacagcggga aggacaagga ttggatata aactcaggca	780
ttcaagccag caacagcaac cccctttggg tcccctccca ttgtatggg gctctgttt	840
cactctat cactctatta aatcatgcaa ctgcactctt ctggccgtg tttttatgg	900
ctcaagctga gctttgttc gccatccacc actgctgttt gccaccgtca cagaccgct	960
gctgacttcc atccctttgg atccagcaga gtgtccactg tgctcctgat ccagcgaggt	1020
acccattgcc actcccgatc aggctaaagg cttgccattg ttccctgcattg gctaagtgcc	1080
tggtttgtc ctaatagaac tgaacactgg tcactgggtt ccatgggtct cttccatgac	1140
ccacggcttc taatagagct ataacactca ccgcatggcc caagattcca ttccttggta	1200
tctgtgaggc caagaacccc aggtcagaga angtgaggct tgccaccatt tgggaagtgg	1260
cccactgcca ttttggtagc ggcaccac catcttggg gctgtggag caaggatccc	1320
ccagtaaca	1329

<210> 13

<211> 162

<212> PRT

<213> MSRV

<220>

<221> misc\_feature

<222> (26)..(26)

<223> Xaa = any amino acid

<220>

<221> misc\_feature

<222> (42)..(42)

<223> Xaa = any amino acid

<220>

<221> misc\_feature

<222> (46)..(46)

<223> Xaa = any amino acid

<400> 13

Gln Asn Arg Arg Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr  
1 5 10 15

Cys Leu Phe Leu Gly Glu Glu Cys Cys Xaa Tyr Val Asn Gln Ser Gly  
20 25 30

Ile Ile Thr Glu Lys Val Lys Glu Ile Xaa Asp Arg Ile Xaa Cys Arg  
35 40 45

Ala Glu Asp Leu Gln Asn Thr Ala Pro Trp Gly Leu Leu Ser Gln Trp  
50 55 60

Met Pro Trp Thr Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Phe  
65 70 75 80

Leu Leu Leu Phe Gly Pro Cys Ile Phe Asn Phe Leu Val Lys Phe Val  
85 90 95

Ser Ser Arg Ile Glu Ala Val Lys Leu Gln Ile Val Leu Gln Met Glu  
100 105 110

Pro Gln Met Gln Ser Met Thr Lys Ile Tyr Arg Gly Pro Leu Asp Arg  
115 120 125

Pro Ala Arg Leu Cys Ser Asp Val Asn Asp Ile Glu Val Thr Pro Pro  
130 135 140

Glu Glu Ile Ser Thr Ala Gln Pro Leu Leu His Ser Asn Ser Val Gly  
145 150 155 160

Ser Ser

<210> 14

<211> 21

<212> DNA

<213> MSRV

<400> 14

ggcattgata gcacccatca g

21

<210> 15

<211> 21

<212> DNA

<213> MSRV

<400> 15

catgtcacca gggtggaata g

21

<210> 16

<211> 758

<212> DNA

<213> MSRV

<400> 16

ggcattgata gcacccatca gatggccaaa tcattattta ctggaccagg cctttcaaa

60

actatcaagc agatagggcc cgtgaagcat gccaaagaaa taatcccctg ccttatcgcc

120

atgttccttc aggagaacaa agaacaggcc attacccagg ggaagactgg caactagatt

180

ttacccacat ggccaaatgt cagggatttc agcatctact agtctggca gatacttca

240

ctgggtgggt ggagtcttct cctttagga cagaaaagac ccaagaggtt ataaaaggcac 300  
taatgaaata attcccgat ttggacttcc cccaggatta cagggtgaca atggccccgc 360  
tttcaaggct gcagtaaccc agggagtatc ccaggtgtt ggcataaat atcacttaca 420  
ctgtgcctgg aggccacaat cctccagaaa agtcaagaaa atgaatgaaa cactcaaaga 480  
tctaaaaaaag ctaacccaag aaacccacat tgcatgacct gttctgttgc ctataacctt 540  
actaagaatc cataactatc ccccaaaaag caggacttag cccatacgag atgctatatg 600  
gatggccttt cctaaccaat gaccttgc ttgactgaga aatggccaac ttagttgcag 660  
acatcacctc ctttagccaaa tatcaacaag ttcttaaaac atcacaggga acctgtcccc 720  
gagaggaggg aaaggaacta ttccaccctg gtgacatg 758

<210> 17

<211> 25

<212> DNA

<213> MSRV

<400> 17  
cggacatcca aagtgtatggg aaacg 25

<210> 18

<211> 26

<212> DNA

<213> MSRV

<400> 18  
ggacaggaaa gtaagactga gaaggc 26

<210> 19

<211> 26

<212> DNA

<213> MSRV

<400> 19  
cctagaacgt attctggaga attggg 26

<210> 20

<211> 26

<212> DNA

<213> MSRV

<400> 20  
tggctctcaa tggtaaaca tacccg 26

<210> 21

<211> 1511

<212> DNA

<213> MSRV.

<400> 21  
cctagaacgt attctggaga attgggacca atgtgacact cagacgctaa gaaagaaacg 60  
atttatattc ttctgcagta ccgcctggcc acaatatcct cttcaaggga gagaaacctg 120  
gcttcctgag ggaagtataa attataacat catcttacag ctagacctct tctgtagaaa 180  
ggagggcaaa tggagtgaag tgccatatgt gcaaacttcc tttcattaa gagacaactc 240  
acaattatgt aaaaagtgtg gtttatgccc tacaggaagc cctcagagtc cacccctta 300  
ccccagcgtc ccctccccga ctccttcctc aactaataag gacccccc tttaacccaa 360  
ggtccaaaag gagatagaca aaggggtaaa caatgaacca aagagtgc 420  
atattccccg attatgcccc ctccaagcag tgagaggagg agaattcggc ccagccagag tgcctgtacc 480  
ttttctctc tcagacttaa agcaaattaa aatagaccta ggtaaattct cagataaccc 540  
tgacggctat attgatgttt tacaagggtt aggacaatcc tttgatctga catggagaga 600  
tataatgtta ctactaaatc agacactaac cccaaatgag agaagtgc 660  
ctgtaactgc agcccgagag tttggcgatc tttggtatct cagtcaggcc aacaatagga tgacaacaga 720  
ggaaagaaca actccccacag gccagcaggc agttcccagt gtagaccctc attgggacac 780  
agaatcagaa catggagatt ggtgccacaa acatttgcta acttgcgtgc tagaaggact 840  
gagggaaaact aggaagaagc ctatgaatta ctcaatgatg tccactataa cacaggaaa 900

ggaagaaaat cttactgctt ttctggacag actaagggag gcattgagga agcataacctc 960  
cctgtcacct gactctattg aaggccaact aatcttaaag gataagttt tcactcagtc 1020  
agctgcagac attagaaaaa acttcaaaag tctgccttag gcccggagca gaacttagaa 1080  
accctattta acttggcattc ctcagtttt tataatagag atcaggagga gcaggcgaaa 1140  
cgggacaaac gggataaaaaa aaaaaggggg ggtccactac ttttagtcatg gccctcaggc 1200  
aagcagactt tggaggctct gcaaaaggaa aaagctggc aaatcaaatg cctaataagg 1260  
ctggcttcca gtgcggtcta caaggacact ttaaaaaaga ttatccaagt agaaataagc 1320  
cgcccccttg tccatgcccc ttacgtcaag ggaatcactg gaaggcccac tgccccaggg 1380  
gatgaagata ctctgagtca gaagccatta accagatgat ccagcagcag gactgagggt 1440  
gccccggggcg agcgccagcc catgccatca ccctcacaga gccccgggta tgtttacca 1500  
ttgagagccaa 1511

<210> 22

<211> 352

<212> PRT

<213> MSRV

<400> 22

Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu  
1 5 10 15

Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr  
20 25 30

Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr  
35 40 45

Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp  
50 55 60

Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser  
65 70 75 80

Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser  
85 90 95

Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn  
100 105 110

Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly  
115 120 125

Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu  
130 135 140

Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro  
145 150 155 160

Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe  
165 170 175

Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln  
180 185 190

Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr  
195 200 205

Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe  
210 215 220

Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu  
225 230 235 240

Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro  
245 250 255

His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu  
260 265 270

Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met  
275 280 285

Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu  
290 295 300

Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser  
305 310 315 320

Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe  
325 330 335

Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro  
340 345 350

<210> 23

<211> 30

<212> DNA

<213> MSRV

<400> 23

tgctggatt cgggatccta gaacgtattc

30

<210> 24

<211> 30

<212> DNA

<213> MSRV

<400> 24

agttctgctc cgaagcttag gcagactttt

30

<210> 25

<211> 398

<212> PRT

<213> MSRV

<400> 25

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
1 5 10 15

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
20 25 30

Ile Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr  
35 40 45

Leu Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln  
50 55 60

Tyr Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn  
65 70 75 80

Tyr Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys  
85 90 95

Trp Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn  
100 105 110

Ser Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln  
115 120 125

Ser Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr  
130 135 140

Asn Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys  
145 150 155 160

Gly Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro  
165 170 175

Leu Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val  
180 185 190

Pro Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys  
195 200 205

Phe Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly  
210 215 220

Gln Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln  
225 230 235 240

Thr Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu  
245 250 255

Phe Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr  
260 265 270

Glu Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp  
275 280 285

Pro His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His  
290 295 300

Leu Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro  
305 310 315 320

Met Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn  
325 330 335

Leu Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr  
340 345 350

Ser Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys  
355 360 365

Phe Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu  
370 375 380

Pro Lys Leu Ala Ala Ala Leu Glu His His His His His His  
385 390 395

<210> 26

<211> 378

<212> PRT

<213> MSRV

<400> 26

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Leu Glu Arg  
1 5 10 15

Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu Arg Lys Lys  
20 25 30

Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr Pro Leu Gln  
35 40 45

Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr Asn Ile Ile  
50 55 60

Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp Ser Glu Val  
65 70 75 80

Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser Gln Leu Cys  
85 90 95

Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser Pro Pro Pro  
100 105 110

Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn Lys Asp Pro  
115 120 125

Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly Val Asn Asn  
130 135 140

Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu Gln Ala Val  
145 150 155 160

Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro Phe Ser Leu  
165 170 175

Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe Ser Asp Asn  
180 185 190

Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln Ser Phe Asp  
195 200 205

Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr Leu Thr Pro  
210 215 220

Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe Gly Asp Leu  
225 230 235 240

Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu Glu Arg Thr  
245 250 255

Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro His Trp Asp  
260 265 270

Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu Leu Thr Cys  
275 280 285

Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met Asn Tyr Ser  
290 295 300

Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu Thr Ala Phe  
305 310 315 320

Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser Leu Ser Pro  
325 330 335

Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe Ile Thr Gln  
340 345 350

Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro Lys Leu Ala  
355 360 365

Ala Ala Leu Glu His His His His His  
370 375

<210> 27

<211> 25

<212> DNA

<213> MSRV

<400> 27

cttggagggt gcataaccag ggaat

25

<210> 28

<211> 20

<212> DNA

<213> MSRV

<400> 28

tgtccgctgt gctcctgatc

20

<210> 29

<211> 25

<212> DNA

<213> MSRV

<400> 29  
ctatgtcctt ttggactgtt tgggt 25

<210> 30

<211> 764

<212> DNA

<213> MSRV

<400> 30  
tgtccgctgt gtcctgatc cagcacaggg gcccattgcc tctcccaatt gggctaaagg 60  
cttgcatttgcata gctaagtgc tgggttcatc ctaatcgagc tgaacactag 120  
tcactgggtt ccacggttct cttccatgac ccatggcttc taatagagct ataacactca 180  
ctgcatggtc caagattcca ttccttggaa tccgtgagac caagaacccc aggtcagaga 240  
acacaaggct tgccaccatg ttggaagcag cccaccacca ttttggaaagc agcccgccac 300  
tatcttggga gctctggag caaggacccc aggttaacaat ttggtgacca cgaaggggacc 360  
tgaatccgca accatgaagg gatctccaaa gcaattggaa atttcctcc caaggcaaaa 420  
atgcccctaa gatgtattct ggagaattgg gaccaatttg accctcagac agtaagaaaa 480  
aaatgactta tattttctg cagtaccgcc ctggccacga tattcttcc aagggggaga 540  
aacctggcct cctgagggaa gtataaatta taacaccatc ttacagctag acctgtttt 600  
tagaaaagga ggcaaattgga gtgaagtgc atatttacaa actttcttt cattaaaaga 660  
caactcgcaa ttatgttaac agtgtgattt gtgttcctac acggaagccc tcagattcta 720  
ctccccaccc ccggcatctc ccctgaatcc ctccccact tatt 764

<210> 31

<211> 800

<212> DNA

<213> MSRV

<400> 31  
tgtccgctgt gtcctgatc cagcacaggg gcccattgcc tctcccaatt gggctaaagg 60

cttgcatttgcaca gctaagggcc tgggttcatc ctaatcgagc tgaacactag 120  
tcactgggtt ccacggttct cttccatgac ccatggcttc taatagagct ataacactca 180  
ctgcattggc caagattcca ttccttggaa tccgtgagac caagaacccc aggtcagaga 240  
acacaaggct tgccaccatg ttggaagcag cccaccacca ttttggaaagc ggcccggcac 300  
tatcttggga gctctggag caaggacccc caggtAACAA ttttggtgacc acgaagggac 360  
ctgaatccgc aaccatgaag ggatctccaa agcaatttggaa aatgttcctc ccaaggcaaa 420  
aatgccccta agatgttattc tggagaatttggaccaatct gaccctcaga cagtaagaaa 480  
aaaaatgact tatattcttc tgcagtaccg cctggccacg gatatcctct tcaaggggaa 540  
gaaacctggc ctcctgaggg aagtataat tataacacca tcttacagct agacctgttt 600  
tgttagaaaag gaggcaaatg gagtgaagtggaccaatcttccaaatggaccaatctt 660  
gacaactcgc aattatgtaa acagtgtgat ttgtgtccta caggaagccc tcagatctac 720  
ctccctaccc cggcatctcc ctgactcctt ccccaactaa taaggaccca cttcagccca 780  
aacagtccaa aaggacatag 800

<210> 32

<211> 65

<212> PRT

<213> MSRV

<400> 32

Pro Met Ala Ser Asn Arg Ala Ile Thr Leu Thr Ala Trp Ser Lys Ile  
1 5 10 15

Pro Phe Leu Gly Ile Arg Glu Thr Lys Asn Pro Arg Ser Glu Asn Thr  
20 25 30

Arg Leu Ala Thr Met Leu Glu Ala Ala His His His Phe Gly Ser Ser  
35 40 45

Pro Pro Leu Ser Trp Glu Leu Trp Glu Gln Gly Pro Gln Val Thr Ile  
50 55 60

Trp  
65

<210> 33

<211> 26

<212> DNA

<213> MSRV

<400> 33

tcatgcaact gcactcttct ggtccg

26

<210> 34

<211> 28

<212> DNA

<213> MSRV

<400> 34

tcttgcacta acctccactg tccgttgg

28

<210> 35

<211> 28

<212> DNA

<213> MSRV

<400> 35

atcccccagt aacaatttgg tgaccacg

28

<210> 36

<211> 31

<212> DNA

<213> MSRV

<400> 36

tcgggtctaa gagggtaactt cctttggtag g

31

<210> 37  
<211> 25  
<212> DNA  
<213> MSRV

<400> 37  
ttacgcaggt ctcagggatg agctt 25

<210> 38  
<211> 33  
<212> DNA  
<213> MSRV

<400> 38  
cggcagtagc agtcttagta tctgaagcag tta 33

<210> 39  
<211> 28  
<212> DNA  
<213> MSRV

<400> 39  
ggtacggagg gtttcatgta gttttgag 28

<210> 40  
<211> 1247  
<212> DNA  
<213> MSRV

<220>  
<221> misc\_feature  
<222> (1240)..(1240)

<223> n = a, g, c or t/u

<220>

<221> misc\_feature

<222> (1246)..(1246)

<223> n = a, g, c or t/u

<400> 40  
atgggcagca gccatcatca tcatcatcac agcagcggcc tggtgccgcg cggcagccat 60  
atggctagca tgactggtgg acagcaaatg ggtcgatcc tagaacgtat tctggagaat 120  
tggaccaat gtgacactca gacgctaaga aagaaacgtat ttatattctt ctgcagtacc 180  
gcctggccac aatatcctct tcaaggaga gaaacctggc ttcctgaggg aagtataaat 240  
tataacatca tcttacagct agacctcttc tgttagaaagg agggcaaatg gagtgaagt 300  
ccatatgtgc aaactttctt ttcattaaga gacaactcac aattatgtaa aaagtgtgg 360  
ttatgcccta caggaagccc tcagagtcca cctccctacc ccagcgtccc ctcccccact 420  
cttcctcaa ctaataagga ccccccctta acccaaacgg tccaaaagga gatagacaaa 480  
gggttaaaca atgaaccaaa gagtgccaat attccccat tatgccccct ccaagcagt 540  
agaggaggag aattcggccc agccagagtg cctgtacctt tttctctctc agacttaaag 600  
caaattaaaa tagacctagg taaattctca gataaccctg acggctatat ttagtttt 660  
caagggttag gacaatcctt ttagtctgaca tggagagata taatgttact actaaatcag 720  
acactaacc caaatgagag aagtggcgct gtaactgcag cccgagagtt tggcgatctt 780  
tggtatctca gtcaggccaa caataggatg acaacagagg aaagaacaac tccccacaggc 840  
cagcaggcag ttcccagtgt agaccctcat tgggacacag aatcagaaca tggagattgg 900  
tgccacaaac atttgctaac ttgcgtgcta gaaggactga ggaaaactag gaagaagcct 960  
atgaattact caatgatgtc cactataaca cagggaaagg aagaaaatct tactgtttt 1020  
ctggacagac taagggaggc attgaggaag catacctccc tgcacacctga ctctattgaa 1080  
ggccaaactaa tcttaaagga taagtttac actcagtcag ctgcagacat tagaaaaaac 1140  
ttcaaaagtc tgcctaagct tgcggccgca ctcgagcacc accaccacca ccactgagat 1200  
ccggctgcta acaaagccc aaaggaagct gagttggtn gtggcna 1247

<210> 41  
<211> 1186  
<212> DNA  
<213> MSRV

<400> 41  
atggctagca tgactggtgg acagcaaatg ggtcggatcc tagaacgtat tctggagaat 60  
tgggaccaat gtgacactca gacgctaaga aagaaacgat ttatattctt ctgcagtacc 120  
gcctggccac aatatcctct tcaaggaga gaaacctggc ttccctgaggg aagtataaat 180  
tataacatca tcttacagct agacctcttc tgttagaaagg agggcaaatg gagtgaagt 240  
ccatatgtgc aaactttctt ttcattaaga gacaactcac aattatgtaa aaagtgtggt 300  
ttatgcccta caggaagccc tcagagtcca cctccctacc ccagcgtccc ctcccccact 360  
ctttcctcaa ctaataagga ccccccctta acccaaacgg tccaaaagga gatagacaaa 420  
gggtaaaca atgaaccaaa gagtgccaat attcccgat tatgccccct ccaagcagtg 480  
agaggaggag aattcggccc agccagagtg cctgtacctt tttctctctc agacttaaag 540  
caaattaaaa tagacctagg taaattctca gataaccctg acggctatat ttagttttt 600  
caagggttag gacaatcctt ttagtgcata tggagagata taatgttact actaaatcag 660  
acactaaccc caaatgagag aagtggcgct gtaactgcag cccgagagtt tggcgatctt 720  
tggtatctca gtcaggccaa caataggatg acaacagagg aaagaacaac tccccacaggc 780  
cagcaggcag ttcccagtgt agaccctcat tgggacacag aatcagaaca tggagattgg 840  
tgccacaaaac atttgctaac ttgcgtgcta gaaggactga ggaaaactag gaagaagcct 900  
atgaattact caatgatgtc cactataaca cagggaaagg aagaaaatct tactgcttt 960  
ctggacagac taagggaggc attgaggaag catacctccc tgtcacctga ctctattgaa 1020  
ggccaactaa tcttaaagga taagtttac actcagtcag ctgcagacat tagaaaaaac 1080  
ttcaaaaagtc tgcctaagct tgcggccgca ctcgagcacc accaccacca ccactgagat 1140  
ccggctgcta acaaagcccg aaaggaagct gagttggctg gtggca 1186

<210> 42  
<211> 2030  
<212> DNA

<213> MSRV

<400> 42  
atggccctcc cttatcatac tttctcttt actgttctct taccccttt cgctctcact 60  
gcacccctc catgctgctg tacaaccagt agctccctt accaagagtt tctatgaaga 120  
acgcggcttc ctggaaatat tgatgccccca tcatatagga gtttatctaa gggaaactcc 180  
accttcactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatt 240  
catgcaaata ctcattattg gacagggaaa atgattaatc ctagttgtcc tggaggactt 300  
ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg gggtgaaatt 360  
caaggtcagg caagagaaaa acaagtaaag gaagcaatct cccaaactgac ccggggacat 420  
agcaccctta gcccctacaa aggactagtt ctctcaaaac tacatgaaac cctccgtacc 480  
catactcgcc tggtgagcct atttaataacc accctcactc ggctccatga ggtctcagcc 540  
caaaacccta ctaactgttg gatgtgcctc cccctgcact tcaggccata cattcaatc 600  
cctgttcctg aacaatggaa caacttcagc acagaaataa acaccacttc cgtttttagta 660  
ggacctcttg tttcaatct ggaataacc catacctcaa acctcacctg tgtaaaattt 720  
agcaatacta tagacacaac cagctcccaa tgcattcagg gggtaacacc tcccacacga 780  
atagtctgcc tacccctcagg aatattttt gtctgtggta cctcagccta tcattgtttg 840  
aatggctctt cagaatctat gtgcttcctc tcattcttag tgccccctat gaccatctac 900  
actgaacaag atttatacaa tcatgtcgta cctaagcccc acaacaaaag agtaccatt 960  
cttcctttg ttatcagagc aggagtgcta ggcagactag gtactggcat tggcagtatc 1020  
acaacctcta ctcagttcta ctacaaacta tctcaagaaa taaatggta catggAACAG 1080  
gtcactgact ccctggtcac cttgcaagat caacttaact ccctagcagc agtagtcctt 1140  
caaaatcgaa gagctttaga cttgctaacc gccaaaagag gggAACCTG tttatTTTA 1200  
ggagaagaac gctgttatta tgttaatcaa tccagaatttgc tcaactgagaa agttaaagaa 1260  
attcgagatc gaatacaatg tagagcagag gagcttcaaa acaccgaacg ctggggcctc 1320  
ctcagccaat ggatgccctg ggttctcccc ttcttaggac ctctagcagc tctaataattt 1380  
ttactcctct ttggaccctg tatcttaac ctccttggta agtttgcctc ttccagaattt 1440  
gaagctgtaa agctacagat ggtcttacaa atggaacccc agatggagtc catgactaag 1500  
atccaccgtg gaccctgga ccggcctgct agcccatgct ccgatgttaa tgacattgaa 1560  
ggcaccctc ccgagggaaat ctcaactgca caaccctac tatgccccaa ttcagcggga 1620

agcagttaga	gcggcatca	gccaacctcc	ccaacagcac	ttgggtttc	ctgttgagag	1680
ggggactga	gagacaggac	tagctggatt	tcctaggcca	acgaagaatc	cctaagccta	1740
gctggaaagg	tgactgcatac	cacctctaaa	catggggctt	gcaacttagc	tcacacccga	1800
ccaatcagag	agctcactaa	aatgctaatt	aggcaaaaat	aggaggtaaa	gaaatagcca	1860
atcatctatt	gcctgagagc	acagcgggag	ggacaaggat	cggatataa	acccagggcat	1920
tcgagccggc	aacggcaacc	cccttgggt	cccctccctt	tgtatggcg	ctctgtttc	1980
actctatttc	actctattaa	atcttgcaac	tgaaaaaaaaa	aaaaaaaaaa		2030

<210> 43

<211> 2055

<212> DNA

<213> MSRV

<400> 43						
cagcaacccc	ctttgggtcc	cctccattg	tatggagct	ctgtttcac	tctatttcac	60
tctattaaat	catgcaactg	cactcttctg	gtccgtgtt	tttatggctc	aagctgagct	120
tttggcgcc	atccaccact	gctgttgcc	accgtcacag	accgctgct	gacttccatc	180
ccttggatc	cagcagagtg	tccgctgtgc	tcctgatcca	gcacaggcgc	ccattgcctc	240
tcccaattgg	gctaaaggct	tgccattgtt	cctgcacagc	taagtgcctg	ggttcatcct	300
aatcgagctg	aacactagtc	actgggttcc	acggttctct	tccatgaccc	atggcttcta	360
atagagctat	aacactcact	gcatggtcca	agattccatt	ccttggaaatc	cgtgagacca	420
agaaccccag	gtcagagaac	acaaggcttg	ccaccatgtt	ggaaggcagcc	caccaccatt	480
tttggaaaggcag	cccgccacta	tcttgggagc	tctggagca	aggaccccag	gtaacaattt	540
ggtgaccacg	aagggacctg	aatccgcaac	catgaaggga	tctccaaagc	aatggaaac	600
gttccccccg	aggcaaaaat	gcccctagaa	cgtattctgg	agaattggga	ccaatgtgac	660
actcagacgc	taagaaagaa	acgatttata	ttcttctgca	gtaccgcctg	gccacaatat	720
cctcttcaag	ggagagaaac	ctggcttcct	gagggaaagta	taaattataa	catcatctta	780
cagctagacc	tcttctgttag	aaaggaggc	aatggagtg	aagtgccata	tgtgcaaact	840
ttcttttcat	taagagacaa	ctcacaatta	tgtaaaaagt	gtggtttatg	ccctacagga	900
agccctcaga	gtccacactcc	ctaccccagc	gtcccctccc	cgactccttc	ctcaactaat	960

aaggaccccc	ctttaaccca	aacggtccaa	aaggagatag	acaaagggg	aaacaatgaa	1020
ccaaagagt	ccaatattcc	ccgattatgc	cccctccaag	cagtgagagg	aggagaattc	1080
ggcccagcca	gagtgcctgt	accttttct	ctctcagact	taaagcaa	taaaatagac	1140
ctaggtaaat	tctcagataa	ccctgacggc	tatattgatg	ttttacaagg	gttaggacaa	1200
tcctttgatc	tgacatggag	agatataatg	ttactactaa	atcagacact	aacccaaat	1260
gagagaagt	ccgctgtaac	tgcagcccga	gagtttggcg	atcttggta	tctcagtcag	1320
gccaacaata	gatgacaac	agaggaaga	acaactccc	caggccagca	ggcagttccc	1380
agttagacc	ctcattggga	cacagaatca	gaacatggag	attggtgcca	caaacattt	1440
ctaacttgcg	tgctagaagg	actgagggaa	actaggaaga	agcctatgaa	ttactcaatg	1500
atgtccacta	taacacaggg	aaaggaagaa	aatcttactg	ctttctgga	cagactaagg	1560
gaggcattga	ggaagcatac	ctccctgtca	cctgactcta	ttgaaggcca	actaatctt	1620
aaggataagt	ttatcactca	gtcagctgca	gacattagaa	aaaaacttca	aaagtccgtc	1680
ttaggctcgg	aacaaaactt	agaaacccta	ttgaacttgg	caacctcggt	ttttataat	1740
agagatcagg	aggagcaggc	agaatggac	aatgggata	aaaaaaaaag	ggccaccgct	1800
ttagtcatgg	ccctcaggca	agcggacttt	ggaggctctg	gaaaaggaa	aagctggca	1860
aataggaagc	ctaatagggc	ttgcttccag	tgcggtctac	aaggacactt	taaaaaagat	1920
tgtccaaata	gaaataagcc	gcccccttgt	ccatgcccct	tacgtcaagg	gaatcactgg	1980
aaggcccact	gccccagggg	atcaagatac	tctgagtcag	aagccattaa	ccagatgatc	2040
cagcagcagg	actga					2055

<210> 44

<211> 1197

<212> DNA

<213> MSRV

<400> 44	ggacccgtag	tatgggtaa	tcccctccgg	gaaaccaagc	cccagtactc	agaagaagaa	60
atagaatggg	gaacctcacg	aggacatggt	ttcctcccct	caggatggct	agccactgaa		120
gaaggaaaaa	tactttgct	ggcagcta	caatggaaat	tacttaaaac	ccttcagcaa		180
accttccact	taggcattga	tagcacccat	cagatagcca	aatcattatt	tactggacca		240

ggcctttca	aaactatcaa	gcagatagtc	agggcctgtg	aagtgtgcca	aagaaataat	300
cccctgcctt	atcgccaagc	tccttcagga	gaacaaagaa	caggcaatta	cccaagagaa	360
gactggcaac	tagatttat	ccacatgcca	aaatcacagg	gatttcagtg	tctactagtc	420
tggtagata	ctttcactgg	ttgggcagag	gccttcccct	gtaggacaga	aaagttccaa	480
gaggtataaa	aggcactagt	tcatgaagta	attcccagat	tcggacttcc	ctgaggctta	540
cagagtgaca	atggcctgc	tttcaaggcc	acagtaaccc	aggagatatc	ccaggcgtta	600
ggtatagaat	atcacttaca	ctgcacctag	aggccacaat	cctcagggaa	ggttgagaaa	660
atgaaaacac	tcaaacgaca	tctaaacaag	ctaaccagg	aaacccacct	cgcattgtct	720
gctctgttgt	ctatagcctt	actaagaatc	caaaactctc	ccaaaaggc	aggacttagc	780
ccatacagaa	tgctgtatgg	acggccttc	ctaaccaatg	accttctgct	tgaccaagag	840
atggccaact	tagttgcaga	catcacctcc	ttagccaaat	atcaacaagt	tctaaaaca	900
ttacaaggag	cctgtcccg	agaggaggga	aaagaaatat	tccaccctgg	tgtcatggta	960
ttagtcaagt	cccttccctc	taattcccc	tccctagaca	catcctgggg	aggaccctac	1020
ccagtcattt	tatctatccc	aactgcggtt	aaagtggctg	gagtgagtc	ttggatacat	1080
cacactcgaa	tcaaaccctg	gatactgccg	aaggaacccg	aaaatccagg	ggacaacgct	1140
agctatttct	ttgaacctct	agaggatctg	tgcctgctct	tcaagcaaca	accgtga	1197

<210> 45

<211> 1718

<212> DNA

<213> MSRV

<400> 45	gagaatagca	gcataagttg	gctggcagaa	gtaggaaag	acagcaagaa	gtaaagaaaa	60
	aaaggagaaa	gtcagagaaa	gaaaaaaaaa	gaggaagaaa	caaagaagaa	cttgaagaga	120
	gaaagaagta	gtaaagaaaa	aacagtatac	cctattcctt	taaaagccag	ggtaaatttc	180
	tgtctaccta	gccaggcat	attcttctta	tgtggAACAT	caacctatat	ctgcctcccc	240
	actaactgga	caggcaccag	aaccttagtc	tttctaagtc	ccaacattaa	cattgcccc	300
	ggaaatcaga	ccctattgg	acctgtcaaa	gctaaagtcc	gtcagtgcag	agccatacaa	360
	ctaataccc	tattatagg	gttaggaatg	gtactgcta	cagaactgg	aatagccggt	420

ttatctactt cattatccta ctaccataca ctctcaaaga atttctcaga cagttgcaa	480
gaaataatga aatctattct tactttacaa tcccaattag actcttggc agcaatgact	540
ctccaaaacc gccgaggccc acacccctc actgctgaga aaggaggact ctgcaccc	600
ttaggggaag agtgttgtt ttacactaac cagtcaggaa tagtacgaga tgccacctgg	660
catttacagg aaagggttc tgatatcaga caatgcctt caaactctta taccaaccc	720
tggagttggg caacatggct tcttccattt ctaggtccca tggcagccat cttgctgtt	780
ctcaccccttggcc gcccctgtat tttaagctt cttgtcaaattt ttgtttccctc taggatcgaa	840
gccatcaagc tacagatggt cttacaaatg gaaccccaaa ttagttcaac taacaacttc	900
taccaaggac ccctggaacg atccactggc acttccacta gcctagagat tcccctctgg	960
aagacactac aactgcaggg ccccttctt gcccctatcc agcaggaagt agctagagcg	1020
gtcatcggcc aaattcccaa cagcagttgg ggtgtcctgt ttagaggggg gattgaagag	1080
tgacagcctg ctggcagcct cacagccctc gttggatctc agtgcctcct cagccttgg	1140
gcccactctg gccgtgcttg aggagccctt cagcctgcca ctgcactgtg ggagcccttt	1200
tctgggctgg acaaggccgg agccagctcc ctcagcttgc agggaggtat ggagggagag	1260
atgcaggcgg gaaccaggc tgcgcatggc gttgcgggc cagcatgagt tccaggtgg	1320
cgtgggctcg gcgggccccca cactcggca gtgagggct tagcacctgg gccagacaga	1380
tgctgtgctc aacttcttcg ctggccctta gctgccttcc ccgtggggca gggctacgg	1440
aacatgcagc ctgccccatgc ttgagccccc cacccggccg tgggttcttg cacagccaa	1500
gcttcccgga caagcaccac cccttatcca cggtgccca tcccatcaac caccaaggg	1560
ttgaggagtg cgggcacaca gcgcgggatt ggcaggcagt tccacttgcg gccttgg	1620
gggatccact gcgtgaagcc agctggctc ctgagtctgg tggggacttg gagaatctt	1680
atgtctagct aaggattgt aaatacacca atcagcac	1718